

Tommy Kaplan, PhD

Contact Address

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Education

- 2002 – 2008 Ph.D. in Computer Science and Computational Biology.**
Thesis entitled “From DNA Sequence to Chromatin Dynamics: Computational Analysis of Transcriptional Regulation” has been approved on July 15th, 2008
School of Computer Science and Faculty of Medicine,
The Hebrew university, Jerusalem, Israel.
- 2000 – 2002 M.Sc. in Computer Science.**
The Hebrew university, Jerusalem, Israel.
(As part of direct studies towards a Ph.D. degree)
- 1998 – 2000 B.Sc. in Computer Science and Cognitive Studies.**
The Hebrew university, Jerusalem, Israel
- 1996 – 1997 B.Sc. studies in Mathematics and Computer Science.**
Tel-Aviv University, Israel.

Awards

- 2009 GE & Science Prize for Young Life Scientists, “Rest of the World”**
regional winner (excluding N. America, Europe and Japan).
- 2008 – 2010 EMBO long-term post-doctoral fellowship**
- 2008 Candidate for the 2008 **ACM Doctoral Dissertation** award, on behalf of**
the School of Computer Science, The Hebrew University of Jerusalem,
Israel.
- 2007 Distinguished Graduate Student prize in **Computer Science and****
Computational Biology. The Hebrew University.
- 2006 Barenholz Prize for Applied Research**
- 2005 – 2008 Leibniz Center for Research in Computer Science student fellowship**
- 2004 Keystone Symposia Scholarship Winner**
- 2002 – 2005 Horwitz Fellowship for Excellent Interdisciplinary Ph.D. students**
- 2002 – 2005 Eshkol Foundation scholarship for Ph.D. students (waived)**
- 2002 Rector’s Award for graduate students**
- 2000 Selim and Rachel Benin Award for undergraduate students**

Professional Experience

- 2002 – 2008** **Teacher** as part of the combined B.Sc/M.Sc program in Computer Science and Life Sciences. School of Computer Science. The Hebrew university.
Courses taught: Workshop in Computational Bioskills; Research Methods in Computational Biology (seminar); Final Research Projects.
- 1999 – 2008** **Research** under the supervision of **Prof. Nir Friedman** – School of Computer Science, and **Prof. Hanah Margalit** – Department of Molecular Genetics and Biotechnology, Faculty of Medicine, The Hebrew university.
- 2001** **Teaching Assistant** in “Computer Architecture” course
School of Computer Science. The Hebrew university.
- 1998 – 2000** UNIX System admin
Racah Institute of Physics, The Hebrew university.
- 1998 – 2000** Large applications engineer (C++). Onset Technology (*Shonut*).
- 1993 – 1998** Algorithmic R+D, teaching and programming. IDF Intelligence Forces.

Publications

Journal Papers

1. Yassour M*, **Kaplan T***, Fraser HB, Levine JZ, Pfiffner J, Adiconis X, Schroth G, Luo S, Khrebtkova I, Gnirke A, Nusbaum N, Thompson DA, Friedman N, and Regev A
ab initio Construction of a Eukaryotic Transcriptome by Massively Parallel mRNA Sequencing
PNAS, 2009, 106(9):3264-9
2. **Kaplan T***, Liu CL*, Erkmann JA*, Holik J, Grunstein M, Kaufman PD, Friedman N and Rando OJ
Cell Cycle- and Chaperone-Mediated Regulation of H3K56ac Incorporation in Yeast
PLoS Genetics, 2008, 4(11):e1000270
3. Capaldi AP, **Kaplan T**, Liu Y, Habib N, Regev A, Friedman N, and O’Shea EK
Structure and Function of a Transcriptional Network Activated by the MAPK Hog1
Nature Genetics, 2008, 40:1300-6
4. Habib N*, **Kaplan T***, Margalit H, and Friedman N
A novel Bayesian DNA motif comparison method for clustering and retrieval.
PLoS Comput Biology, 4(2): e1000010, 2008
5. Dion MF*, **Kaplan T***, Kim M, Buratowski S, Friedman N, and Rando OJ
Dynamics of replication-independent histone turnover in budding yeast
Science, 315(5817):1405-8, 2007
6. Liu CL*, **Kaplan T***, Kim M, Buratowski S, Schreiber SL, Friedman N, and Rando OJ
Single-Nucleosome Mapping of Histone Modifications in *S. cerevisiae*
PLoS Biology, 3(10): e328, 2005
7. **Kaplan T**, Friedman N and Margalit H
ab initio Prediction of Transcription Factor Targets using Structural Knowledge
PLoS Computational Biology, 2005, 1(1):e1
8. Barash Y*, Elidan G*, **Kaplan T***, and Friedman N
CIS: Compound Importance Sampling Method for Transcription Factor Site *p*-value Estimation
Bioinformatics, 21(5):596:600, 2005
9. Friedberg I, **Kaplan T** and Margalit H
Evaluation of PSI-BLAST alignment Accuracy in Comparison to Structural Alignments.
Protein Science, 2000, (11):2278-84

Peer-reviewed Conference Proceedings

10. Yassour M, **Kaplan T**, Jaimovich A, and Friedman N
Nucleosome Positioning from Tiling Microarray Data. *Proc. Int. Sys. Comp. Biol. (ISMB)*, 2008
11. **Kaplan T**, Friedman N and Margalit H
Predicting Transcription Factor Binding Sites Using Structural Knowledge
Proc. Of the 9th Ann. Int. Conf. in Comp. Mol. Bio. (RECOMB), 2005
12. Barash Y*, Elidan G*, **Kaplan T***, and Friedman N
CIS: Compound Importance Sampling Method for Transcription Factor Site p-value Estimation
Short Paper. *Proc. Int. Sys. Comp. Biol. (ISMB)*, 2004
13. Barash Y*, Elidan G*, Friedman N, and **Kaplan T***
Modeling Dependencies in Protein-DNA Binding Sites
Proc. Of the 7th Ann. Int. Conf. in Comp. Mol. Bio. (RECOMB), 2003
14. Friedberg I, **Kaplan T** and Margalit H
Glimmers in the Midnight Zone: Characterization of Aligned Identical Residues in Sequence-Dissimilar Proteins Sharing a Common Fold
Proc. Int. Sys. Comp. Biol. (ISMB), 2000: 162-170

Technical Reports

15. Habib N*, **Kaplan T***, Margalit H, Friedman N
DNA Motif Analysis Tools Based on a Novel Motif Similarity Score
TR-2007-55, School of Computer Science and Engineering, The Hebrew University.
16. **Kaplan T** and Friedman N
Model-Based Analysis of High-Resolution Chromatin Immunoprecipitation Data
TR-2006-11, School of Computer Science and Engineering, The Hebrew University.

Selected Posters:

1. 11th Israeli Bioinformatics Symposium 2008. **Best Poster Runner-up.**
Dynamics of Replication-Independent Histone Turnover in Budding Yeast
2. Hebrew University Open Day 2007. **Best Poster Award.**
Dynamics of Replication-Independent Histone Turnover in Budding Yeast
3. Hebrew University Open Day 2005. **Best Poster Award.**
Analyzing DNA sequence motifs in a SNAP
4. Keystone symposium on Biological Discovery Using High-Throughput Data, 2004. **The Keystone Symposia Scholarship Winner.**
Using Structural Knowledge for *ab initio* Prediction of Transcription Factor Targets.
5. *Proc. Int. Sys. Comp. Biol. (ISMB)*, 2002. **Best Poster Award.**
Using Structure and Sequence Information for Predicting Transcription Factor Binding Sites
6. *Israel Bioinformatics Symposium*, 2001. **Best Poster Award**
Determination of Key Positions in Distantly Related Proteins

References

1. **Prof. Michael B. Eisen** (Post-doctoral Advisor)
Howard Hughes Medical Institute; and the Department of Molecular and Cell Biology, QB3 Institute, University of California, Berkeley, CA, USA. mbeisen@berkeley.edu, <http://rana.lbl.gov/eisen>
2. **Prof. Nir Friedman** (Ph.D. Advisor).
School of Computer Science and Engineering, The Hebrew University of Jerusalem, Israel. nir@cs.huji.ac.il, <http://www.cs.huji.ac.il/~nir>

3. **Prof. Hanah Margalit** (Ph.D. Advisor).
Department of Molecular Genetics and Biotechnology, Faculty of Medicine, The Hebrew University of Jerusalem, Israel. hanah@md.huji.ac.il, <http://margalit.huji.ac.il>
4. **Prof. Aviv Regev** (Collaborator).
Howard Hughes Medical Institute; The Department of Biology, Massachusetts Institute of Technology; and The Broad Institute of MIT and Harvard, Cambridge, MA, USA. aregev@broad.mit.edu, <http://www.broad.mit.edu/about/bios/bio-regev.html>
5. **Prof. Oliver J. Rando** (Collaborator).
The Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, USA. Oliver.Rando@umassmed.edu, <http://www.umassmed.edu/bmp/faculty/rando.cfm>